

m. masher

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TECH CENTER 1600/2900



#6

RAW SEQUENCE LISTING

DATE: 03/04/2002

PATENT APPLICATION: US/09/724,392

TIME: 15:03:50

Input Set : N:\Crif3\RULE60\09724392.txt

Output Set: N:\CRF3\03042002\I724392.raw

4 <110> APPLICANT: Moore, K.
5 Nagle, D.
6 Woolf, E.
8 <120> TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
11 <130> FILE REFERENCE: 7853-119
13 <140> CURRENT APPLICATION NUMBER: 09/724,392
14 <141> CURRENT FILING DATE: 2000-11-28
16 <150> PRIOR APPLICATION NUMBER: 09/062,753
17 <151> PRIOR FILING DATE: 1998-04-17
19 <150> PRIOR APPLICATION NUMBER: 08/833,226
20 <151> PRIOR FILING DATE: 1997-04-17
22 <160> NUMBER OF SEQ ID NOS: 8
24 <170> SOFTWARE: FastSEQ for Windows Version 3.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 4052
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (45)...(1196)
35 <400> SEQUENCE: 1

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37		Met Ala Ala Gln
38		1
40	aat gga aac acc agt ttc aca ccc aac ttt aat cca ccc caa gac cat	104
41	Asn Gly Asn Thr Ser Phe Thr Pro Asn Phe Asn Pro Pro Gln Asp His	
42	5 10 15 20	
44	gcc tcc tcc ctc tcc ttt aac ttc agt tat ggt gat tat gac ctc cct	152
45	Ala Ser Ser Leu Ser Phe Asn Phe Ser Tyr Gly Asp Tyr Asp Leu Pro	
46	25 30 35	
48	atg gat gag gat gag gac atg acc aag acc cgg acc ttc ttc gca gcc	200
49	Met Asp Glu Asp Glu Asp Met Thr Lys Thr Arg Thr Phe Phe Ala Ala	
50	40 45 50	
52	aag atc gtc att ggc att gca ctg gca ggc atc atg ctg gtc tgc ggc	248
53	Lys Ile Val Ile Gly Ile Ala Leu Ala Gly Ile Met Leu Val Cys Gly	
54	55 60 65	
56	atc ggt aac ttt gtc ttt atc gct gcc ctc acc cgc tat aag aag ttg	296
57	Ile Gly Asn Phe Val Phe Ile Ala Ala Leu Thr Arg Tyr Lys Lys Leu	
58	70 75 80	
61	cgc aac ctc acc aat ctg ctc att gcc aac ctg gcc atc tcc gac ttc	344
62	Arg Asn Leu Thr Asn Leu Leu Ile Ala Asn Leu Ala Ile Ser Asp Phe	
63	85 90 95 100	
65	ctg gtg gcc atc atc tgc tgc ccc ttc gag atg gac tac tac gtg gta	392

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66	Leu Val Ala Ile Ile Cys Cys Pro Phe Glu Met Asp Tyr Tyr Val Val	
67	105 110 115	
69	cgg cag ctc tcc tgg gag cat ggc cac gtg ctc tgt gcc tcc gtc aac	440
70	Arg Gln Leu Ser Trp Glu His Gly His Val Leu Cys Ala Ser Val Asn	
71	120 125 130	
73	tac ctg cgc acc gtc tcc ctc tac gtc tcc acc aat gcc ttg ctg gcc	488
74	Tyr Leu Arg Thr Val Ser Leu Tyr Val Ser Thr Asn Ala Leu Leu Ala	
75	135 140 145	
77	att gcc att gac aga tat ctc gcc atc gtt cac ccc ttg aaa cca cgg	536
78	Ile Ala Ile Asp Arg Tyr Leu Ala Ile Val His Pro Leu Lys Pro Arg	
79	150 155 160	
81	atg aat tat caa acg gcc tcc ttc ctg atc gcc ttg gtc tgg atg gtg	584
82	Met Asn Tyr Gln Thr Ala Ser Phe Leu Ile Ala Leu Val Trp Met Val	
83	165 170 175 180	
85	tcc att ctc att gcc atc cca tcg gct tac ttt gca aca gaa acc gtc	632
86	Ser Ile Leu Ile Ala Ile Pro Ser Ala Tyr Phe Ala Thr Glu Thr Val	
87	185 190 195	
89	ctc ttt att gtc aag agc cag gag aag atc ttc tgt ggc cag atc tgg	680
90	Leu Phe Ile Val Lys Ser Gln Glu Lys Ile Phe Cys Gly Gln Ile Trp	
91	200 205 210	
93	cct gtg gat cag cag ctc tac tac aag tcc tac ttc ctc ttc atc ttt	728
94	Pro Val Asp Gln Gln Leu Tyr Tyr Lys Ser Tyr Phe Leu Phe Ile Phe	
95	215 220 225	
97	ggt gtc gag ttc gtg ggc cct gtg gtc acc atg acc ctg tgc tat gcc	776
98	Gly Val Glu Phe Val Gly Pro Val Val Thr Met Thr Leu Cys Tyr Ala	
99	230 235 240	
101	agg atc tcc cgg gag ctc tgg ttc aag gca gtc cct ggg ttc cag acg	824
102	Arg Ile Ser Arg Glu Leu Trp Phe Lys Ala Val Pro Gly Phe Gln Thr	
103	245 250 255 260	
105	gag cag att cgc aag cgg ctg cgc tgc cgc agg aag acg gtc ctg gtg	872
106	Glu Gln Ile Arg Lys Arg Leu Arg Cys Arg Arg Lys Thr Val Leu Val	
107	265 270 275	
109	ctc atg tgc att ctc acg gcc tat gtg ctg tgc tgg gca ccc ttc tac	920
110	Leu Met Cys Ile Leu Thr Ala Tyr Val Leu Cys Trp Ala Pro Phe Tyr	
111	280 285 290	
113	ggt ttc acc atc gtt cgt gac ttc ttc ccc act gtg ttc gtg aag gaa	968
114	Gly Phe Thr Ile Val Arg Asp Phe Phe Pro Thr Val Phe Val Lys Glu	
115	295 300 305	
118	aag cac tac ctc act gcc ttc tac gtg gtc gag tgc atc gcc atg agc	1016
119	Lys His Tyr Leu Thr Ala Phe Tyr Val Val Glu Cys Ile Ala Met Ser	
120	310 315 320	
122	aac agc atg atc aac acc gtg tgc ttc gtg acg gtc aag aac aac acc	1064
123	Asn Ser Met Ile Asn Thr Val Cys Phe Val Thr Val Lys Asn Asn Thr	
124	325 330 335 340	
126	atg aag tac ttc aag aag atg atg ctg ctg cac tgg cgt ccc tcc cag	1112
127	Met Lys Tyr Phe Lys Lys Met Met Leu Leu His Trp Arg Pro Ser Gln	
128	345 350 355	
130	cgg ggg agc aag tcc agt gct gac ctt gac ctc aga acc aac ggg gtg	1160
131	Arg Gly Ser Lys Ser Ser Ala Asp Leu Asp Leu Arg Thr Asn Gly Val	

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132	360	365	370	
134	ccc acc aca gaa gaa gtg gac tgt atc agg ctg aag tgacccactg			1206
135	Pro Thr Thr Glu Glu Val Asp Cys Ile Arg Leu Lys			
136	375	380		
138	gtgtcacaca attgaaaacc ccagtcacagt actcagagca tcacccacca tcaaccaagt			1266
139	tcataggctg catgggaaat gacatctgtg ttcatgctc ccccggtgcc tcaagaagcc			1326
140	gaatgctgca aagtcgtaac atacaatgag actagacatg aaccaaataca gctgacattt			1386
141	actgatatcc gctcgacacc tactgtgtcc acaatcccca caaggagatt agacacaagg			1446
142	agcagcaact gacatggact gaacatgtac tgtgtgcaaa ccacaccaat gagattagac			1506
143	ggggacagca ggagctgaca ttactcttc acctactgta atcaaaaaca cttgatttga			1566
144	ttacaatcaa aaacatataa aaaacataac aaagtagcag aagctatttg agtttccaag			1626
145	ctatctccag atatatagat agttcacccct ccactctccc taattctgta tcttaccagt			1686
146	gcaggaatat caaaaggcta taggccaggc atgatggctc atgacctgta tcccagcact			1746
147	tggggaggct gaggcacgtg gatcacttga ggtcaggagt tcaaccagg ctggccaaca			1806
148	tggtgaaacc ctgtctctac taaaaataca aaattagcta ggcgtggtgg cgggcgcctg			1866
149	taatcccagt tactcaggag gctgaagcag gagaatagct tgaacctggg agttggagtt			1926
150	tgacgtgagc tgagattgct ccactgcact ccagcctgag tgacagagtg agactctgtc			1986
151	tcaggaaaaa aacaaacaaa caaacaacaa aacaacaaca acaacaacaa caaccaacgg			2046
152	ctatagaaga agactcttcg acacaatgga aatgtaacga taagtttgtc agtgcgtggt			2106
153	ttacagcatc atgggagggtg cgttacagcc atcatactga actttcccac ccacctccta			2166
154	ctgcctccca gggcattctc taggattttg gcttcaagaa aaaaaaatt cttatagtca			2226
155	gccagcctt atgtggttat ccacaatggt gtaatttcaa aggaaagaac ctaaaaatca			2286
156	ctttcccact gatgcttgaa agcttatcat tttatttggg tggagatggg taatcctgag			2346
157	gtgtcaattt ttgcctctc agtgcaaagg atttcagtg cctcggggtc agggggaaag			2406
158	aggacagaga aaaaagtgga gggtgccact ggcaatgaac ataactctctg tgggcatttt			2466
159	gctaaggact ggaccacttt ctagaacact ccctctttta caaaaggaaac tctacctaga			2526
160	atccaaagac ctgggttcag gtcctaactc taagactcaa gtcctaaatt catgatgttt			2586
161	tctctctgtg tctcagtttt gctttaatga aatggcgtat atgaaaatat ctgctcttca			2646
162	taccttgcaa gactgttggg agagcccatt gaggccatgg tttgtgaatg tgcttttcaa			2706
163	ctgtgcacac gataagaatg gagaagtgat attgaacagt ttatttggag ggagtttatt			2766
164	tggaaacccc atccactgtg atttattaga gaaataccca cactttttca tccctgttct			2826
165	ttggatgaaa gactcctgaa gacttcacag tgtaccttgt ctacagtggg ccaaaaaggg			2886
166	atccctgttc ttggttataa tctgggaaat ttaacctcag attctcagtg accccaagac			2946
167	tctcagcatc cctgcggtct tagaagtgtt gacagcttct cctgcatgtt gcaaaaatagc			3006
168	accctagtgc tgcataaata tcaacttctga atctgtttgt attattatac atttgtggta			3066
169	actgtaggta cacgtcttca tttcttcttg attcattttg atgtggtagc tatgcaaatg			3126
170	gtacctgggt tgggactgac ccattccatat ttgaccaatt cctaattttt tatagacaag			3186
171	gaattaattg tttgcttgtt tgattgtttc tattatttgt tgatttgttt ctctgactga			3246
172	agtttcaacc aatgtttctt tctatcacca cccagcagac tcaccttcag cccaatcatt			3306
173	gtactctcag aaaatgcagg ccggcatggt ggctcacatc tgtaatccca gcacttcggg			3366
174	aggccaagat gggcagatca cctgagggtca ggagttcaag accagcctgg ccaacatggc			3426
175	aaaaccccat ctctagaaaa atacagaaat tagctggcgt ggtggcacat gcctgtggtc			3486
176	ccagctcctc aggaggctga ggcattgagaa ttgcttgaac cccagaggca gaggttgag			3546
177	tgaattgaga tgcaccact gcactccagc ctgggtgata gagcaagatt ccatctcaaa			3606
178	aggaaaataa aagaaaatgc aaacacata taatattagc ctaagcaaaa ctgttaattc			3666
179	tgatttacaa aaattcttac ttgcttggct ttgaaatgca ttgtgtaata atgcatttca			3726
180	aagccaagca agtaacaatt ttaggttatg tacatttcta taaatataat aattgtattt			3786
181	ttatttatta ttctatcctg gctcttagcc gaatcaggag attctttagg aatggaccat			3846
182	gtaccagtca agtctgtcag caggattcat caccctgttc ctttttgtcc tagaatatac			3906

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183 caacttcctt tcattgaaat ttaactgaaa aaacttttgt aaatatcagt gtgtatttgt 3966
184 gattttccag tgattaaaagt gtgatgttgt tatccaatta aataattaac atgtggaatt 4026
185 taaaaaaaaa aaaaaagggc ggccgc 4052
187 <210> SEQ ID NO: 2
188 <211> LENGTH: 384
189 <212> TYPE: PRT
190 <213> ORGANISM: Homo sapiens
192 <400> SEQUENCE: 2
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194 1 5 10 15
195 Pro Gln Asp His Ala Ser Ser Leu Ser Phe Asn Phe Ser Tyr Gly Asp
196 20 25 30
197 Tyr Asp Leu Pro Met Asp Glu Asp Glu Asp Met Thr Lys Thr Arg Thr
198 35 40 45
199 Phe Phe Ala Ala Lys Ile Val Ile Gly Ile Ala Leu Ala Gly Ile Met
200 50 55 60
201 Leu Val Cys Gly Ile Gly Asn Phe Val Phe Ile Ala Ala Leu Thr Arg
202 65 70 75 80
203 Tyr Lys Lys Leu Arg Asn Leu Thr Asn Leu Leu Ile Ala Asn Leu Ala
204 85 90 95
205 Ile Ser Asp Phe Leu Val Ala Ile Ile Cys Cys Pro Phe Glu Met Asp
206 100 105 110
207 Tyr Tyr Val Val Arg Gln Leu Ser Trp Glu His Gly His Val Leu Cys
208 115 120 125
209 Ala Ser Val Asn Tyr Leu Arg Thr Val Ser Leu Tyr Val Ser Thr Asn
210 130 135 140
211 Ala Leu Leu Ala Ile Ala Ile Asp Arg Tyr Leu Ala Ile Val His Pro
212 145 150 155 160
213 Leu Lys Pro Arg Met Asn Tyr Gln Thr Ala Ser Phe Leu Ile Ala Leu
214 165 170 175
215 Val Trp Met Val Ser Ile Leu Ile Ala Ile Pro Ser Ala Tyr Phe Ala
216 180 185 190
217 Thr Glu Thr Val Leu Phe Ile Val Lys Ser Gln Glu Lys Ile Phe Cys
218 195 200 205
219 Gly Gln Ile Trp Pro Val Asp Gln Gln Leu Tyr Tyr Lys Ser Tyr Phe
220 210 215 220
221 Leu Phe Ile Phe Gly Val Glu Phe Val Gly Pro Val Val Thr Met Thr
222 225 230 235 240
223 Leu Cys Tyr Ala Arg Ile Ser Arg Glu Leu Trp Phe Lys Ala Val Pro
224 245 250 255
225 Gly Phe Gln Thr Glu Gln Ile Arg Lys Arg Leu Arg Cys Arg Arg Lys
226 260 265 270
227 Thr Val Leu Val Leu Met Cys Ile Leu Thr Ala Tyr Val Leu Cys Trp
228 275 280 285
229 Ala Pro Phe Tyr Gly Phe Thr Ile Val Arg Asp Phe Phe Pro Thr Val
230 290 295 300
231 Phe Val Lys Glu Lys His Tyr Leu Thr Ala Phe Tyr Val Val Glu Cys
232 305 310 315 320
234 Ile Ala Met Ser Asn Ser Met Ile Asn Thr Val Cys Phe Val Thr Val

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235          325          330          335
236 Lys Asn Asn Thr Met Lys Tyr Phe Lys Lys Met Met Leu Leu His Trp
237          340          345          350
238 Arg Pro Ser Gln Arg Gly Ser Lys Ser Ser Ala Asp Leu Asp Leu Arg
239          355          360          365
240 Thr Asn Gly Val Pro Thr Thr Glu Glu Val Asp Cys Ile Arg Leu Lys
241          370          375          380
243 <210> SEQ ID NO: 3
244 <211> LENGTH: 3317
245 <212> TYPE: DNA
246 <213> ORGANISM: Mus musculus
248 <220> FEATURE:
249 <221> NAME/KEY: CDS
250 <222> LOCATION: (269)...(1411)
252 <400> SEQUENCE: 3
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254 ggcgatcttt gggagaccaa tagacgcccc agagggagga cactgggatc cagactccac      120
255 tggaaccccc cttttcagat cctggatggt atctgttctc cctaaggatt ctaacaggga      180
256 cctgcactca ctgaccccag cagaagtgtc gaactccacg tgagcgcata tccctgatac      240
257 acaccagccc acctgtagca tcataaac atg gga ccc cag aac aga aac act      292
258                               Met Gly Pro Gln Asn Arg Asn Thr
259                               1           5
261 agc ttt gca cca gac ttg aat cca ccc caa gac cat gtc tcc tta aac      340
262 Ser Phe Ala Pro Asp Leu Asn Pro Pro Gln Asp His Val Ser Leu Asn
263 10           15           20
265 tac agt tat ggt gat tat gac ctc ccc ctg ggt gag gat gag gat gtg      388
266 Tyr Ser Tyr Gly Asp Tyr Asp Leu Pro Leu Gly Glu Asp Glu Asp Val
267 25           30           35           40
269 acc aag aca cag acc ttc ttt gca gcc aaa att gtc att ggc gtg gca      436
270 Thr Lys Thr Gln Thr Phe Phe Ala Ala Lys Ile Val Ile Gly Val Ala
271          45           50           55
273 ctg gca ggc atc atg ctg gtc tgc ggc att ggc aac ttt gtc ttc att      484
274 Leu Ala Gly Ile Met Leu Val Cys Gly Ile Gly Asn Phe Val Phe Ile
275          60           65           70
277 gct gcc ctc gcc cgc tac aag aag ctg cgc aac ctt acc aac ctc ctc      532
278 Ala Ala Leu Ala Arg Tyr Lys Lys Leu Arg Asn Leu Thr Asn Leu Leu
279          75           80           85
281 att gct aac ctg gcc atc tct gac ttc ctg gtg gcg atc gtc tgc tgc      580
282 Ile Ala Asn Leu Ala Ile Ser Asp Phe Leu Val Ala Ile Val Cys Cys
283          90           95          100
285 ccc ttt gag atg gac tat tat gta gta cgg cag ctt tcc tgg gcg cat      628
286 Pro Phe Glu Met Asp Tyr Tyr Val Val Arg Gln Leu Ser Trp Ala His
287 105          110          115          120
289 ggt cac gtg ctt tgt gcc tcc gtc aac tac ctt cgt acg gtc tcc ctg      676
290 Gly His Val Leu Cys Ala Ser Val Asn Tyr Leu Arg Thr Val Ser Leu
291          125          130          135
293 tac gtc tcc acc aac gct ctg ctg gcc atc gct att gac aga tac ctc      724
294 Tyr Val Ser Thr Asn Ala Leu Leu Ala Ile Ala Ile Asp Arg Tyr Leu
295          140          145          150

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VERIFICATION SUMMARY

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